Schematic representation of EIA virus S2 gene and mutant clones derived from EIAV_UK. The EIA proviral DNA is shown at the top; the complete deduced amino acid sequence of the putative S2 protein is shown in single letter amino acid code at the bottom. Stop codons (indicated by arrows) were introduced into various positions in the EIA virus S2 gene to generate the specific mutant virus strains.
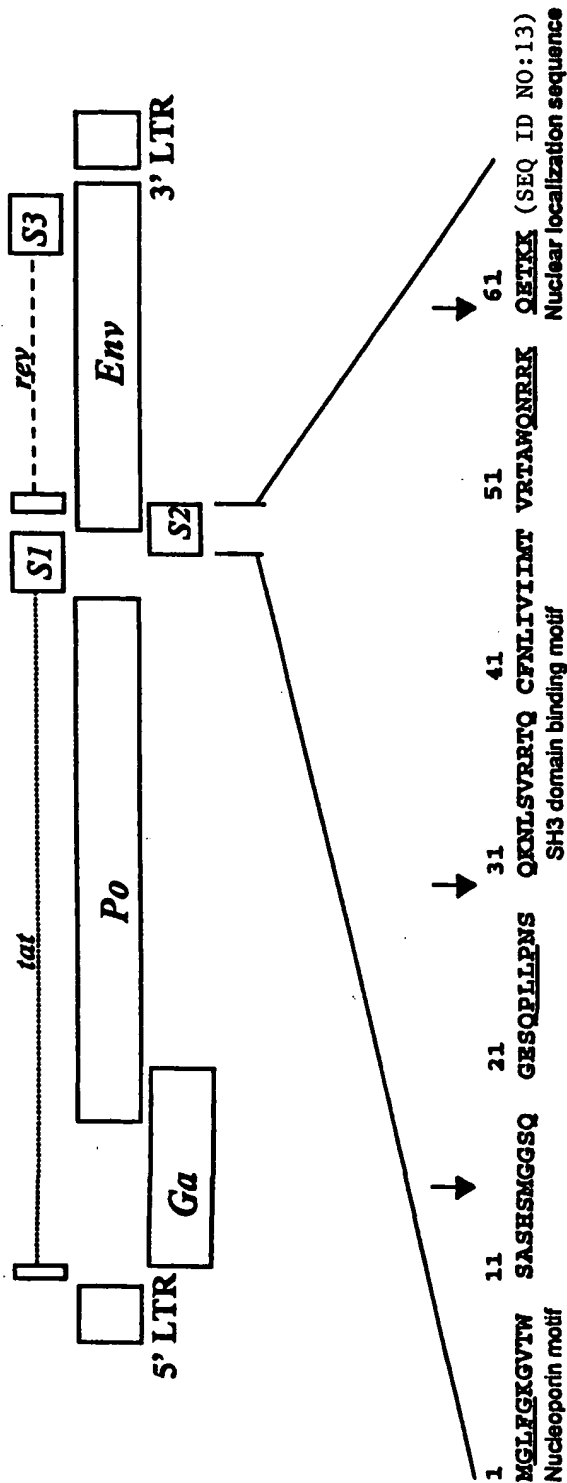

1			
MGLEGKGVTW			
Nucleoporin motif			

11   21   31   41   51   61

SASHSMGGSQ   GESQPLLPNS   QKNLSVRRTQ   CFNLIVIIMT   VRTAWQNRRK   QETKK (SEQ ID NO:13)

SH3 domain binding motif   Nuclear localization sequence

EIAV.G5/s   Stop codon replaced amino acid G⁵

EIAV.2M/X   M¹⁶ changed to T

Stop codons replaced G⁵ and G¹⁸

EIAV.ΔS2   Deletion of initial 5 nucleotides of S2

FIG. 2a

Schematic representation of the Wild-type EIAV *S2* gene compared with the Δ *S2* gene of EIAV.2M/X (EIAV$_{IIK}$ΔS2)
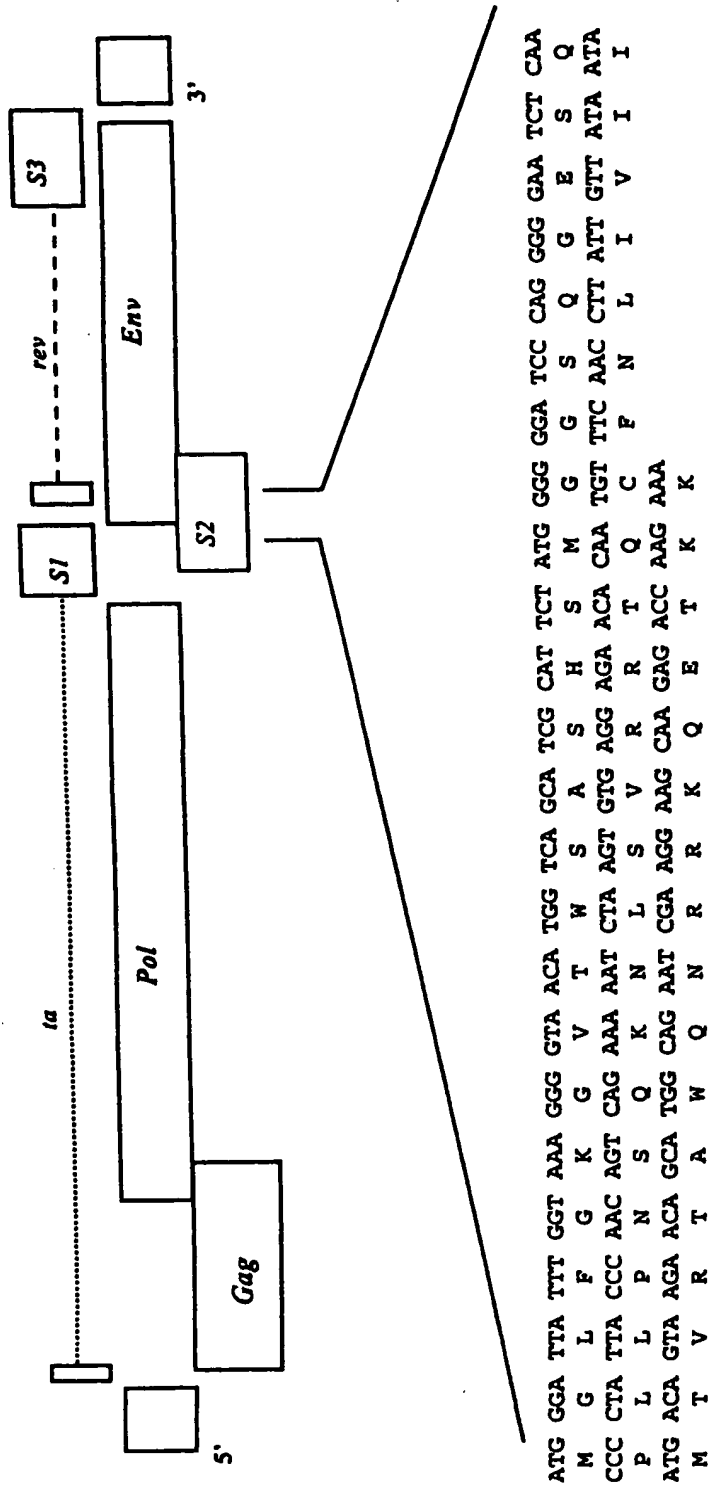
(SEQ ID NO:14)
Wild type

```
ATG GGA TTA TTT GGT AAA GGG GTA ACA TGG TCA GCA TCG CAT TCT ATG GGG GGA TCC CAG GGG GAA TCT CAA
 M   G   L   F   G   K   G   V   T   W   S   A   S   H   S   M   G   G   S   Q   G   E   S   Q
CCC CTA TTA CCC AAC AGT GTG AGG ACA TGT TTC AAC CTT ATT GTT ATA ATA
 P   L   L   P   N   S   V   R   T   Q   C   F   N   L   I   V   I   I
ATG ACA GTA AGA ACA GCA TGG CAG AAT CGA AGG AAG CAA GAG ACC AAG AAA
 M   T   V   R   T   A   W   Q   N   R   R   K   Q   E   T   K   K
```

(SEQ ID NO:15)
ΔS2

```
ATG GGA GTA TAC TAG TGT AAA GGG GTA ACA TGG TCA GCA TCG CAT TCT ACG GGG TGA TCC CAG GGG GAA TCT
 M   G   V   Y   •   C   K   G   V   T   W   S   A   S   H   S   T   G   •   S   Q   G   E   S
CAA CCC CTA TTA CCC AAC AGT CAG AAA AAT CTA AGT GTG AGG ACA CAA TGT TTC AAC CTT ATT GNT ATA
 Q   P   L   L   P   N   S   Q   K   N   L   S   V   R   T   Q   C   F   N   L   I   V   I
ATA ATG ACA GTA AGA ACA GCA TGG CAG AAT CGA AGG AAG CAA GAG ACC AAG AAA
 I   M   T   V   R   T   A   W   Q   N   R   R   K   Q   E   T   K   K
```
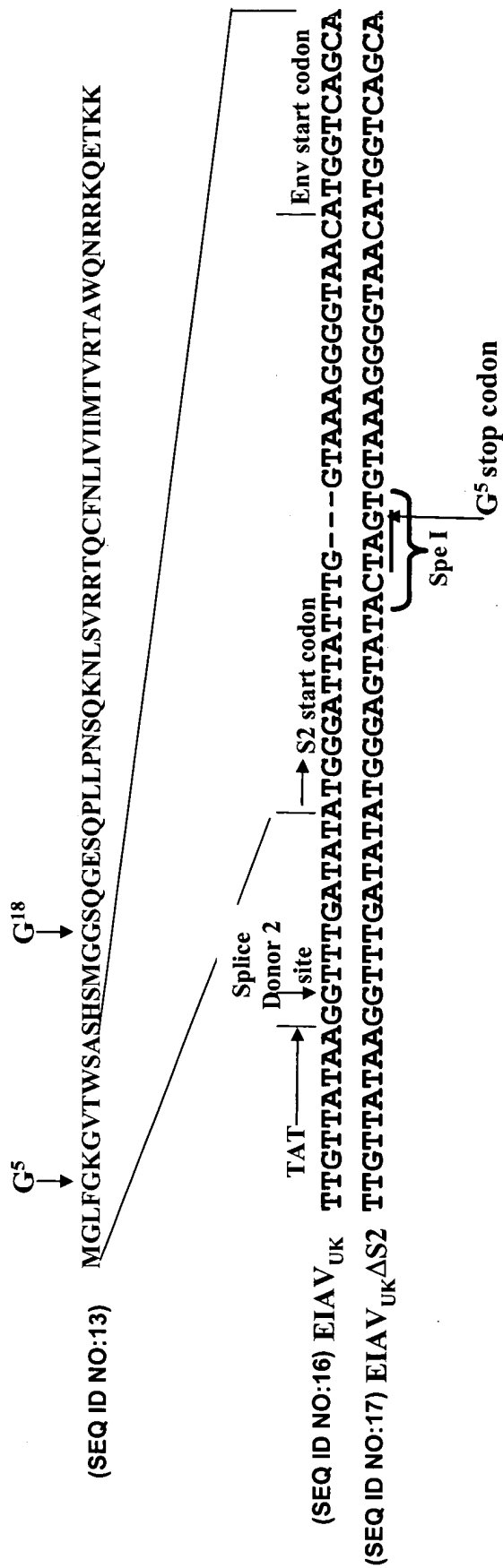
FIG. 2b

REPLACEMENT SHEET

$G^5 \rightarrow$ $G^{18} \rightarrow$

(SEQ ID NO:13) MGLFGKGVTWSASHSMGGSQGESQPLLPNSQKNLSVRRTQCFNLIVIMTVRTAWQNRRKQETKK

Splice Donor 2 site $\rightarrow$ S2 start codon | Env start codon

TAT $\rightarrow$

(SEQ ID NO:16) EIAV$_{UK}$ TTGTTATAAGGTTTGATATATGGGATTATTTG---GTAAAGGGGTAACATGGTCAGCA

(SEQ ID NO:17) EIAV$_{UK}\Delta$S2   TTGTTATAAGGTTTGATATATGGGAGTATACTAGTGTAAAGGGGTAACATGGTCAGCA

Spe I G^5 stop codon

FIGURE 6

(SEQ ID NO:17) ΔS2: TTGTTATAAGGTTTGATATATGGGAGTATACTAGTGTAAAGGGGTAACATGGTCAGCA

(SEQ ID NO:18) D14: TTGTTATAAGGTTT-------------TACTAGTGTAAAGGGGTAACATGGTCAGCA

(SEQ ID NO:19) D25: TTGTTATAAGGTTT-------------TACTAGT-------ACATGGTCAGCA

FIGURE 7

(SEQ ID NO:17) ΔS2 : TTGTTATAAGGTTTGATATATGGGAGTATACTAGTGTAAAGGGGTAACATGGTCAGCA

(SEQ ID NO:20) D6 : TTGTTATAAGGTTTGA-----GGAGTATACTAGTGTAAAGGGGTAACATGGTCAGCA

(SEQ ID NO:21) D9 : TTGTTATAAGGTTTGA--------GTATACTAGTGTGTAAAGGGGTAACATGGTCAGCA

FIGURE 9